



SEQUENCE LISTING

46

<110> Cornell Research Foundation

Chang, Yung-Fu

PE Jr

<120> Ehrlichia canis Genes for Vaccine Development

<130> CRF 2322 CIP

<160> 13

<170> PatentIn version 3.1

<210> 1

<211> 5299

<212> DNA

<213> Ehrlichia canis

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<221> gene

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<210> 2

<211> 522

<212> DNA

<213> *Ehrlichia canis*

<220>

<221> CDS

<222> (1)..(522)

<223> Protein translated from nucleotides 12 through 533 (cytochrome oxidase homolog).

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1

5

10

15

cta tct atg ata tgt tta gtg tac gct tct gta cca cta tat agt ata 96

Leu Ser Met Ile Cys Leu Val Tyr Ala Ser Val Pro Leu Tyr Ser Ile

20

25

30

ttt tgt aaa gta aca ggt tat gga ggt aca gta aga aca agt aat ata 144
Phe Cys Lys Val Thr Gly Tyr Gly Thr Val Arg Thr Ser Asn Ile
35 40 45

tca aat tct aaa ata ggt aac act att att aaa gtc aga ttt aat gca 192
Ser Asn Ser Lys Ile Gly Asn Thr Ile Ile Lys Val Arg Phe Asn Ala
50 55 60

gat ata cac aaa caa ctg cca tgg aaa ttc tat cca gaa gta tct cat 240
Asp Ile His Lys Gln Leu Pro Trp Lys Phe Tyr Pro Glu Val Ser His
65 70 75 80

gta ttt gta aaa cca gga gaa caa aaa ttg att ttc tac cgc gca gaa 288
Val Phe Val Lys Pro Gly Glu Gln Lys Leu Ile Phe Tyr Arg Ala Glu
85 90 95

aat cta ctt gat gag gac act tca gga atg gct gta tat aat gtt aca 336
Asn Leu Leu Asp Glu Asp Thr Ser Gly Met Ala Val Tyr Asn Val Thr
100 105 110

cca cat aaa gta gga aaa tat ttt aat aag gta gct tgt ttt tgt ttc 384
Pro His Lys Val Gly Lys Tyr Phe Asn Lys Val Ala Cys Phe Cys Phe
115 120 125

acc aaa caa aca tta tac cct cat caa aaa act ata atg cca gta tca 432
Thr Lys Gln Thr Leu Tyr Pro His Gln Lys Thr Ile Met Pro Val Ser
130 135 140

ttt ttt ata gat cca gcc ata gaa aca gat cct gaa act gct gac gta 480
Phe Phe Ile Asp Pro Ala Ile Glu Thr Asp Pro Glu Thr Ala Asp Val
145 150 155 160

aaa ctc atc act ctt tca tat gta ttc ttt aag tac aaa gaa 522
Lys Leu Ile Thr Leu Ser Tyr Val Phe Phe Lys Tyr Lys Glu
165 170

<210> 3

<211> 174

<212> PRT

<213> Ehrlichia canis

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Leu Ser Met Ile Cys Leu Val Tyr Ala Ser Val Pro Leu Tyr Ser Ile
20 25 30

Phe Cys Lys Val Thr Gly Tyr Gly Gly Thr Val Arg Thr Ser Asn Ile
35 40 45

Ser Asn Ser Lys Ile Gly Asn Thr Ile Ile Lys Val Arg Phe Asn Ala

50

55

60

Asp Ile His Lys Gln Leu Pro Trp Lys Phe Tyr Pro Glu Val Ser His

65

70

75

80

Val Phe Val Lys Pro Gly Glu Gln Lys Leu Ile Phe Tyr Arg Ala Glu

85

90

95

Asn Leu Leu Asp Glu Asp Thr Ser Gly Met Ala Val Tyr Asn Val Thr

100

105

110

Pro His Lys Val Gly Lys Tyr Phe Asn Lys Val Ala Cys Phe Cys Phe

115

120

125

Thr Lys Gln Thr Leu Tyr Pro His Gln Lys Thr Ile Met Pro Val Ser

130

135

140

Phe Phe Ile Asp Pro Ala Ile Glu Thr Asp Pro Glu Thr Ala Asp Val

145

150

155

160

Lys Leu Ile Thr Leu Ser Tyr Val Phe Phe Lys Tyr Lys Glu

165

170

<210> 4

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<212> DNA

<213> Ehrlichia canis

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<221> CDS

<222> (1)..(1314)

<223> Protein translated from nucleotides 939 through 2,252 (ProA).

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1

5

10

15

aat cat gct tta tcc ttt aac att aaa gtt aca cat gaa aaa tta gat 96

Asn His Ala Leu Ser Phe Asn Ile Lys Val Thr His Glu Lys Leu Asp

20

25

30

aat gga atg gaa gta tac gtg att cca aat cat cgc gca cca gca gtc 144

Asn Gly Met Glu Val Tyr Val Ile Pro Asn His Arg Ala Pro Ala Val

35

40

45

atg cac atg gta tta tac aaa gtc ggt gga act gat gat cca gta gga 192
Met His Met Val Leu Tyr Lys Val Gly Gly Thr Asp Asp Pro Val Gly
50 55 60

tac tct gga tta gca cat ttt ttt gaa cac tta atg ttt agt gga aca 240
Tyr Ser Gly Leu Ala His Phe Phe Glu His Leu Met Phe Ser Gly Thr
65 70 75 80

gaa aaa ttt cct aat ctc atc agc aca ctt agt aat ata ggc gga aat 288
Glu Lys Phe Pro Asn Leu Ile Ser Thr Leu Ser Asn Ile Gly Gly Asn
85 90 95

ttc aat gca agc aca tct caa ttt tgt act ata tac tac gaa tta ata 336
Phe Asn Ala Ser Thr Ser Gln Phe Cys Thr Ile Tyr Tyr Glu Leu Ile
100 105 110

cca aaa caa tat tta tct ctt gca atg gat att gaa tca gac aga atg 384
Pro Lys Gln Tyr Leu Ser Leu Ala Met Asp Ile Glu Ser Asp Arg Met
115 120 125

cag aat ttt aag gtt acc gac aaa gca tta ata aga gaa caa aag gta 432
Gln Asn Phe Lys Val Thr Asp Lys Ala Leu Ile Arg Glu Gln Lys Val
130 135 140

gtc tta gaa gaa aga aaa atg aga gtt gaa agc caa gca aaa aac ata 480
Val Leu Glu Glu Arg Lys Met Arg Val Glu Ser Gln Ala Lys Asn Ile
145 150 155 160

cta gaa gaa gaa atg gaa aat gca ttt tat tac aat gga tat ggc aga 528
Leu Glu Glu Glu Met Glu Asn Ala Phe Tyr Tyr Asn Gly Tyr Gly Arg
165 170 175

cca gta gta gga tgg gaa cat gaa att agc aac tac aac aaa gaa gtt 576
Pro Val Val Gly Trp Glu His Glu Ile Ser Asn Tyr Asn Lys Glu Val
180 185 190

gct gaa gcc ttt cat aag cta cat tat agt cct aat aat gct ata tta 624
Ala Glu Ala Phe His Lys Leu His Tyr Ser Pro Asn Asn Ala Ile Leu
195 200 205

att gta act gga gat gca gat cca caa gaa gta atc aca ctt gca aaa 672
Ile Val Thr Gly Asp Ala Asp Pro Gln Glu Val Ile Thr Leu Ala Lys
210 215 220

caa tac tat ggg aaa ata cca tct aat aat aag aaa cct tca agt caa 720
Gln Tyr Tyr Gly Lys Ile Pro Ser Asn Asn Lys Pro Ser Ser Gln
225 230 235 240

gtt agg gta gaa cca ccg cat aaa aca aat atg act tta aca tta aaa 768
Val Arg Val Glu Pro Pro His Lys Thr Asn Met Thr Leu Thr Leu Lys
245 250 255

gac agt tca gta gaa atc cca gaa ctg ttt tta atg tat caa ata cca 816
Asp Ser Ser Val Glu Ile Pro Glu Leu Phe Leu Met Tyr Gln Ile Pro
260 265 270

aat ggt att acc aat aaa aac tac ata ctt aac atg atg tta gca gaa 864
Asn Gly Ile Thr Asn Lys Asn Tyr Ile Leu Asn Met Met Leu Ala Glu
275 280 285

ata ctc ggt agt ggt aaa ttc agc ctg ctt tac aat gat ttg gta att 912
Ile Leu Gly Ser Gly Lys Phe Ser Leu Leu Tyr Asn Asp Leu Val Ile
290 295 300

aac aat cca ata gtt aca tcg ata aaa aca gat tat aat tac tta act 960
Asn Asn Pro Ile Val Thr Ser Ile Lys Thr Asp Tyr Asn Tyr Leu Thr
305 310 315 320

gac agc gat aat tac ctt tcc att gaa gct ata cct aaa aac ggg atc 1008
Asp Ser Asp Asn Tyr Leu Ser Ile Glu Ala Ile Pro Lys Asn Gly Ile
325 330 335

tct aca gaa gct gta gaa caa gaa att cat aaa tgt ata aat aat tat 1056
Ser Thr Glu Ala Val Glu Gln Glu Ile His Lys Cys Ile Asn Asn Tyr
340 345 350

tta gaa aat gga att tca gca gaa tat tta gaa agt gca aag tat aaa 1104
Leu Glu Asn Gly Ile Ser Ala Glu Tyr Leu Glu Ser Ala Lys Tyr Lys
355 360 365

gta aaa gca cat tta act tat gca ttt gac gga cta act ttc ata tca 1152
Val Lys Ala His Leu Thr Tyr Ala Phe Asp Gly Leu Thr Phe Ile Ser
370 375 380

tat ttt tat ggc atg cat cta ata cta gga gta ccg cta tca gaa atc 1200
Tyr Phe Tyr Gly Met His Leu Ile Leu Gly Val Pro Leu Ser Glu Ile
385 390 395 400

agt aat att tac gat acc ata gac aaa gta agt atc caa gat gtt aac 1248
Ser Asn Ile Tyr Asp Thr Ile Asp Lys Val Ser Ile Gln Asp Val Asn
405 410 415

tcc gct atg gaa aat atc ttt caa aac aat ata aga tta acc ggg cat 1296
Ser Ala Met Glu Asn Ile Phe Gln Asn Asn Ile Arg Leu Thr Gly His
420 425 430

tta tta cct aat gga gaa 1314
Leu Leu Pro Asn Gly Glu
435

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<211> 438

<212> PRT

<213> Ehrlichia canis

<400> 5

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1 5 10 15

Asn His Ala Leu Ser Phe Asn Ile Lys Val Thr His Glu Lys Leu Asp

20

25

30

Asn Gly Met Glu Val Tyr Val Ile Pro Asn His Arg Ala Pro Ala Val

35

40

45

Met His Met Val Leu Tyr Lys Val Gly Gly Thr Asp Asp Pro Val Gly

50

55

60

Tyr Ser Gly Leu Ala His Phe Phe Glu His Leu Met Phe Ser Gly Thr

65

70

75

80

Glu Lys Phe Pro Asn Leu Ile Ser Thr Leu Ser Asn Ile Gly Gly Asn

85

90

95

Phe Asn Ala Ser Thr Ser Gln Phe Cys Thr Ile Tyr Tyr Glu Leu Ile

100

105

110

Pro Lys Gln Tyr Leu Ser Leu Ala Met Asp Ile Glu Ser Asp Arg Met

115

120

125

Gln Asn Phe Lys Val Thr Asp Lys Ala Leu Ile Arg Glu Gln Lys Val

130

135

140

Val Leu Glu Glu Arg Lys Met Arg Val Glu Ser Gln Ala Lys Asn Ile

145

150

155

160

Leu Glu Glu Glu Met Glu Asn Ala Phe Tyr Tyr Asn Gly Tyr Gly Arg

165

170

175

Pro Val Val Gly Trp Glu His Glu Ile Ser Asn Tyr Asn Lys Glu Val

180

185

190

Ala Glu Ala Phe His Lys Leu His Tyr Ser Pro Asn Asn Ala Ile Leu

195

200

205

Ile Val Thr Gly Asp Ala Asp Pro Gln Glu Val Ile Thr Leu Ala Lys

210

215

220

Gln Tyr Tyr Gly Lys Ile Pro Ser Asn Asn Lys Lys Pro Ser Ser Gln

225

230

235

240

Val Arg Val Glu Pro Pro His Lys Thr Asn Met Thr Leu Thr Leu Lys

245

250

255

Asp Ser Ser Val Glu Ile Pro Glu Leu Phe Leu Met Tyr Gln Ile Pro

260

265

270

Asn Gly Ile Thr Asn Lys Asn Tyr Ile Leu Asn Met Met Leu Ala Glu

275

280

285

Ile Leu Gly Ser Gly Lys Phe Ser Leu Leu Tyr Asn Asp Leu Val Ile

290

295

300

Asn Asn Pro Ile Val Thr Ser Ile Lys Thr Asp Tyr Asn Tyr Leu Thr

305

310

315

320

Asp Ser Asp Asn Tyr Leu Ser Ile Glu Ala Ile Pro Lys Asn Gly Ile

325

330

335

Ser Thr Glu Ala Val Glu Gln Glu Ile His Lys Cys Ile Asn Asn Tyr

340

345

350

Leu Glu Asn Gly Ile Ser Ala Glu Tyr Leu Glu Ser Ala Lys Tyr Lys

355

360

365

Val Lys Ala His Leu Thr Tyr Ala Phe Asp Gly Leu Thr Phe Ile Ser

370

375

380

Tyr Phe Tyr Gly Met His Leu Ile Leu Gly Val Pro Leu Ser Glu Ile

385

390

395

400

Ser Asn Ile Tyr Asp Thr Ile Asp Lys Val Ser Ile Gln Asp Val Asn

405

410

415

Ser Ala Met Glu Asn Ile Phe Gln Asn Asn Ile Arg Leu Thr Gly His

420

425

430

Leu Leu Pro Asn Gly Glu

435

<210> 6

<211> 1353

<212> DNA

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<220>

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<222> (1) .. (1353)

<223> Protein translated from nucleotides 2,258 through 3,610 (ProB).

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1 5 10 15

aat aca tat gca aat gat ctc aat att aac ata aaa gaa gct aca act 96

Asn Thr Tyr Ala Asn Asp Leu Asn Ile Asn Ile Lys Glu Ala Thr Thr

20 25 30

aaa aat aaa ata cac tat cta tat gtt gaa cat cat aac cta cca aca 144

Lys Asn Lys Ile His Tyr Leu Tyr Val Glu His His Asn Leu Pro Thr

35 40 45

att tcc tta aaa ttt gca ttc aag aaa gca gga tac gct tat gat gcc 192

Ile Ser Leu Lys Phe Ala Phe Lys Lys Ala Gly Tyr Ala Tyr Asp Ala

50 55 60

ttt gat aag caa gga ctt gca tac ttt aca tca aaa ata tta aac gaa 240

Phe Asp Lys Gln Gly Leu Ala Tyr Phe Thr Ser Lys Ile Leu Asn Glu

65 70 75 80

gga tca aaa aac aac tat gct ctc agt ttt gca caa caa tta gaa ggc 288
Gly Ser Lys Asn Asn Tyr Ala Leu Ser Phe Ala Gln Gln Leu Glu Gly
85 90 95

aaa ggt ata gac tta aaa ttt gat ata gac cta gac aat ttt tat ata 336
Lys Gly Ile Asp Leu Lys Phe Asp Ile Asp Leu Asp Asn Phe Tyr Ile
100 105 110

tca tta aaa acc tta tca gaa aac ttt gaa gaa gcc cta gtt tta ctc 384
Ser Leu Lys Thr Leu Ser Glu Asn Phe Glu Glu Ala Leu Val Leu Leu
115 120 125

agt gat tgc ata ttc aac acc gtc aca gat caa gaa ata ttc aat aga 432
Ser Asp Cys Ile Phe Asn Thr Val Thr Asp Gln Glu Ile Phe Asn Arg
130 135 140

ata ata gca gaa cag att gca cat gtt aaa tca tta tat tct gct cct 480
Ile Ile Ala Glu Gln Ile Ala His Val Lys Ser Leu Tyr Ser Ala Pro
145 150 155 160

gaa ttt ata gct aca aca gaa atg aat cac gct ata ttc aaa ggg cac 528
Glu Phe Ile Ala Thr Thr Glu Met Asn His Ala Ile Phe Lys Gly His
165 170 175

cca tat tct aac aaa gtt tac ggg aca tta aat aca atc aat aat atc 576
Pro Tyr Ser Asn Lys Val Tyr Gly Thr Leu Asn Thr Ile Asn Asn Ile
180 185 190

aac cag gaa gac gtt gca tta tat ata aaa aat agt ttt gac aag gaa 624
Asn Gln Glu Asp Val Ala Leu Tyr Ile Lys Asn Ser Phe Asp Lys Glu
195 200 205

caa atc gtt atc agc gca gca gga gat gta gat cca aca cag cta tca 672
Gln Ile Val Ile Ser Ala Ala Gly Asp Val Asp Pro Thr Gln Leu Ser
210 215 220

aat tta cta gat aaa tat att ctt tcc aaa ttg cca tct ggt aat aac 720
Asn Leu Leu Asp Lys Tyr Ile Leu Ser Lys Leu Pro Ser Gly Asn Asn
225 230 235 240

aaa aat acc ata cca gat acg act gtt aat aga gaa gac aca tta tta 768
Lys Asn Thr Ile Pro Asp Thr Thr Val Asn Arg Glu Asp Thr Leu Leu
245 250 255

tat gta cag aga gat gta cca caa agt gtc ata atg ttt gct aca gac 816
Tyr Val Gln Arg Asp Val Pro Gln Ser Val Ile Met Phe Ala Thr Asp
260 265 270

aca gta cca tat cac agc aaa gac tat cat gca tca aac ttg ttc aat 864
Thr Val Pro Tyr His Ser Lys Asp Tyr His Ala Ser Asn Leu Phe Asn
275 280 285

act atg cta ggc gga tta agt ctc aat tca ata tta atg ata gaa tta 912
Thr Met Leu Gly Gly Leu Ser Leu Asn Ser Ile Leu Met Ile Glu Leu
290 295 300

aga gac aag tta gga tta aca tac cat agt agc agt tca cta tct aac 960
Arg Asp Lys Leu Gly Leu Thr Tyr His Ser Ser Ser Ser Leu Ser Asn
305 310 315 320

atg aat cat agt aat gtg cta ttt ggt aca ata ttc act gat aat acc 1008
Met Asn His Ser Asn Val Leu Phe Gly Thr Ile Phe Thr Asp Asn Thr
325 330 335

aca gta aca aaa tgt ata tcc gtc tta aca gat att ata gag cac att 1056
Thr Val Thr Lys Cys Ile Ser Val Leu Thr Asp Ile Ile Glu His Ile
340 345 350

aaa aag tat gga gtt gat gaa gac act ttt gca att gca aaa tct agt 1104
Lys Lys Tyr Gly Val Asp Glu Asp Thr Phe Ala Ile Ala Lys Ser Ser
355 360 365

att acc aac tct ttt att tta tct atg tta aat aac aat aat gtt agt 1152
Ile Thr Asn Ser Phe Ile Leu Ser Met Leu Asn Asn Asn Val Ser
370 375 380

gag ata ttg tta agc tta caa tta cac gat cta gat ccg agt tat att 1200
Glu Ile Leu Leu Ser Leu Gln Leu His Asp Leu Asp Pro Ser Tyr Ile
385 390 395 400

aat aaa tac aat tct tac tac aaa gca ata aca ata gaa gaa gta aat 1248
Asn Lys Tyr Asn Ser Tyr Tyr Lys Ala Ile Thr Ile Glu Glu Val Asn
405 410 415

aaa att gcc aag aaa att tta tct aat gaa tta gta ata att gaa gta 1296
Lys Ile Ala Lys Lys Ile Leu Ser Asn Glu Leu Val Ile Ile Glu Val
420 425 430

gga aaa aac aat aac ata aat ggc aaa caa ata gat gct aaa aaa cac 1344
Gly Lys Asn Asn Asn Ile Asn Gly Lys Gln Ile Asp Ala Lys Lys His
435 440 445

ata ctt ggt 1353
Ile Leu Gly
450

<210> 7
<211> 451
<212> PRT
<213> Ehrlichia canis

<400> 7

Met Arg Asn Ile Leu Cys Tyr Thr Leu Ile Leu Ile Phe Phe Ser Phe
1 5 10 15

Asn Thr Tyr Ala Asn Asp Leu Asn Ile Asn Ile Lys Glu Ala Thr Thr
20 25 30

Lys Asn Lys Ile His Tyr Leu Tyr Val Glu His His Asn Leu Pro Thr

35

40

45

Ile Ser Leu Lys Phe Ala Phe Lys Lys Ala Gly Tyr Ala Tyr Asp Ala

50

55

60

Phe Asp Lys Gln Gly Leu Ala Tyr Phe Thr Ser Lys Ile Leu Asn Glu

65

70

75

80

Gly Ser Lys Asn Asn Tyr Ala Leu Ser Phe Ala Gln Gln Leu Glu Gly

85

90

95

Lys Gly Ile Asp Leu Lys Phe Asp Ile Asp Leu Asp Asn Phe Tyr Ile

100

105

110

Ser Leu Lys Thr Leu Ser Glu Asn Phe Glu Glu Ala Leu Val Leu Leu

115

120

125

Ser Asp Cys Ile Phe Asn Thr Val Thr Asp Gln Glu Ile Phe Asn Arg

130

135

140

Ile Ile Ala Glu Gln Ile Ala His Val Lys Ser Leu Tyr Ser Ala Pro

145 150 155 160

Glu Phe Ile Ala Thr Thr Glu Met Asn His Ala Ile Phe Lys Gly His

165 170 175

Pro Tyr Ser Asn Lys Val Tyr Gly Thr Leu Asn Thr Ile Asn Asn Ile

180 185 190

Asn Gln Glu Asp Val Ala Leu Tyr Ile Lys Asn Ser Phe Asp Lys Glu

195 200 205

Gln Ile Val Ile Ser Ala Ala Gly Asp Val Asp Pro Thr Gln Leu Ser

210 215 220

Asn Leu Leu Asp Lys Tyr Ile Leu Ser Lys Leu Pro Ser Gly Asn Asn

225 230 235 240

Lys Asn Thr Ile Pro Asp Thr Thr Val Asn Arg Glu Asp Thr Leu Leu

245 250 255

Tyr Val Gln Arg Asp Val Pro Gln Ser Val Ile Met Phe Ala Thr Asp

260

265

270

Thr Val Pro Tyr His Ser Lys Asp Tyr His Ala Ser Asn Leu Phe Asn

275

280

285

Thr Met Leu Gly Gly Leu Ser Leu Asn Ser Ile Leu Met Ile Glu Leu

290

295

300

Arg Asp Lys Leu Gly Leu Thr Tyr His Ser Ser Ser Ser Leu Ser Asn

305

310

315

320

Met Asn His Ser Asn Val Leu Phe Gly Thr Ile Phe Thr Asp Asn Thr

325

330

335

Thr Val Thr Lys Cys Ile Ser Val Leu Thr Asp Ile Ile Glu His Ile

340

345

350

Lys Lys Tyr Gly Val Asp Glu Asp Thr Phe Ala Ile Ala Lys Ser Ser

355

360

365

Ile Thr Asn Ser Phe Ile Leu Ser Met Leu Asn Asn Asn Asn Val Ser

370

375

380

Glu Ile Leu Leu Ser Leu Gln Leu His Asp Leu Asp Pro Ser Tyr Ile

385

390

395

400

Asn Lys Tyr Asn Ser Tyr Tyr Lys Ala Ile Thr Ile Glu Glu Val Asn

405

410

415

Lys Ile Ala Lys Lys Ile Leu Ser Asn Glu Leu Val Ile Ile Glu Val

420

425

430

Gly Lys Asn Asn Asn Ile Asn Gly Lys Gln Ile Asp Ala Lys Lys His

435

440

445

Ile Leu Gly

450

<210> 8

<211> 663

<212> DNA

<213> Ehrlichia canis

<220>

<221> CDS

<222> (1) .. (663)

<223> Protein translated from nucleotides 4,132 through 4,794 (mmpA).

<400> 8

atg aaa gct cat agc aca agt ata cgg aac ttt cag cct tta gaa aga 48

Met Lys Ala His Ser Thr Ser Ile Arg Asn Phe Gln Pro Leu Glu Arg

1 5 10 15

gct gct ata atc att gca gtg tta ggt tta gct gca ttc ttg ttt gct 96

Ala Ala Ile Ile Ile Ala Val Leu Gly Leu Ala Ala Phe Leu Phe Ala

20 25 30

gct gct gcc tgc agt gat cgt ttc caa aga ttg caa tta aca aat cca 144

Ala Ala Ala Cys Ser Asp Arg Phe Gln Arg Leu Gln Leu Thr Asn Pro

35 40 45

ttt gta ata gca gga atg gtt ggc ctt gca gtt ctt tta gtt gct tcc 192

Phe Val Ile Ala Gly Met Val Gly Leu Ala Val Leu Leu Val Ala Ser

50 55 60

tta aca gca gca tta agt ata tgc tta act aaa agt aag caa gtc aca 240

Leu Thr Ala Ala Leu Ser Ile Cys Leu Thr Lys Ser Lys Gln Val Thr

65 70 75 80

caa cat gct att aga cat cgc ttt gga tac gag tca agc act tct tct 288
Gln His Ala Ile Arg His Arg Phe Gly Tyr Glu Ser Ser Thr Ser Ser
85 90 95

tct gta ctg ctt gca ata tca ata att tct tta tta ctt gct gca gca 336
Ser Val Leu Leu Ala Ile Ser Ile Ile Ser Leu Leu Leu Ala Ala Ala
100 105 110

ttt tgt gga aag ata atg ggt aat gac aac cca gat cta ttc ttt agc 384
Phe Cys Gly Lys Ile Met Gly Asn Asp Asn Pro Asp Leu Phe Phe Ser
115 120 125

aag atg caa gaa ctc tcc aat cca ctt gtt gtt gca gct att gta gcc 432
Lys Met Gln Glu Leu Ser Asn Pro Leu Val Val Ala Ala Ile Val Ala
130 135 140

gtt tct gtt ttc cta ctc tca ttc gta atg tat gct gca aag aac att 480
Val Ser Val Phe Leu Leu Ser Phe Val Met Tyr Ala Ala Lys Asn Ile
145 150 155 160

ata agt cca gat aaa caa act cac gtt att ata tta tct aat caa caa 528
Ile Ser Pro Asp Lys Gln Thr His Val Ile Ile Leu Ser Asn Gln Gln
165 170 175

act ata gaa gaa gca aaa gta gat caa gga atg aat att ttg tca gca 576
Thr Ile Glu Glu Ala Lys Val Asp Gln Gly Met Asn Ile Leu Ser Ala
180 185 190

gta ctc cca gca gct ggc att gac atc atg act ata gct tct tgt gac 624
Val Leu Pro Ala Ala Gly Ile Asp Ile Met Thr Ile Ala Ser Cys Asp
195 200 205

att tta gca gtg agc agc cgg gga tcc tct cag cat caa 663
Ile Leu Ala Val Ser Ser Arg Gly Ser Ser Gln His Gln
210 215 220

<210> 9
<211> 221
<212> PRT
<213> Ehrlichia canis

<400> 9

Met Lys Ala His Ser Thr Ser Ile Arg Asn Phe Gln Pro Leu Glu Arg
1 5 10 15

Ala Ala Ile Ile Ile Ala Val Leu Gly Leu Ala Ala Phe Leu Phe Ala
20 25 30

Ala Ala Ala Cys Ser Asp Arg Phe Gln Arg Leu Gln Leu Thr Asn Pro
35 40 45

Phe Val Ile Ala Gly Met Val Gly Leu Ala Val Leu Leu Val Ala Ser

50

55

60

Leu Thr Ala Ala Leu Ser Ile Cys Leu Thr Lys Ser Lys Gln Val Thr

65

70

75

80

Gln His Ala Ile Arg His Arg Phe Gly Tyr Glu Ser Ser Thr Ser Ser

85

90

95

Ser Val Leu Leu Ala Ile Ser Ile Ile Ser Leu Leu Leu Ala Ala Ala

100

105

110

Phe Cys Gly Lys Ile Met Gly Asn Asp Asn Pro Asp Leu Phe Phe Ser

115

120

125

Lys Met Gln Glu Leu Ser Asn Pro Leu Val Val Ala Ala Ile Val Ala

130

135

140

Val Ser Val Phe Leu Leu Ser Phe Val Met Tyr Ala Ala Lys Asn Ile

145

150

155

160

Ile Ser Pro Asp Lys Gln Thr His Val Ile Ile Leu Ser Asn Gln Gln

165

170

175

Thr Ile Glu Glu Ala Lys Val Asp Gln Gly Met Asn Ile Leu Ser Ala

180

185

190

Val Leu Pro Ala Ala Gly Ile Asp Ile Met Thr Ile Ala Ser Cys Asp

195

200

205

Ile Leu Ala Val Ser Ser Arg Gly Ser Ser Gln His Gln

210

215

220

<210> 10

<211> 417

<212> DNA

<213> *Ehrlichia canis*

<220>

<221> CDS

<222> (1) .. (417)

<223> Protein translated from complementary sequence derived from nucleotides 4,883 through 5,299 (partial lipoprotein signal peptidase homolog).

<400> 10

gat cag gta agt aaa tgg tat gta gta aat ttg ata gga gat aaa ggt 48
Asp Gln Val Ser Lys Trp Tyr Val Val Asn Leu Ile Gly Asp Lys Gly

1 5 10 15

gta ata gag ata tta agc ttc ttg cgc ttt act aca gtg tgg aat cct 96
Val Ile Glu Ile Leu Ser Phe Leu Arg Phe Thr Thr Val Trp Asn Pro

20 25 30

gga att agt ttt ggt ata tta aat aac ttt gaa tat agt aat gtt gtt 144
Gly Ile Ser Phe Gly Ile Leu Asn Asn Phe Glu Tyr Ser Asn Val Val

35 40 45

ttt tgt agt atc tcg att ttg att act tgt gtt tta tgc tac tta ttt 192
Phe Cys Ser Ile Ser Ile Leu Ile Thr Cys Val Leu Cys Tyr Leu Phe

50 55 60

ata gta cag cca cat tat aga tta cct ctt gta atc att att ggg ggg 240
Ile Val Gln Pro His Tyr Arg Leu Pro Leu Val Ile Ile Ile Gly Gly

65 70 75 80

tca ata gga aat atc ata gat aga ata aga tat ggt gct gtc tat gat 288
Ser Ile Gly Asn Ile Ile Asp Arg Ile Arg Tyr Gly Ala Val Tyr Asp

85 90 95

ttt ata gat ttt tat atc aat aac tta cat tgg cct gta ttc aac ctg 336

Phe Ile Asp Phe Tyr Ile Asn Asn Leu His Trp Pro Val Phe Asn Leu

100

105

110

gcg gat tct ttt ata ttt tta ggt ata gta ata ata atg gca aag agt 384

Ala Asp Ser Phe Ile Phe Leu Gly Ile Val Ile Ile Met Ala Lys Ser

115

120

125

aat aac cac atg aaa caa att aac tgt aac tcc 417

Asn Asn His Met Lys Gln Ile Asn Cys Asn Ser

130

135

<210> 11

<211> 139

<212> PRT

<213> *Ehrlichia canis*

<400> 11

Asp Gln Val Ser Lys Trp Tyr Val Val Asn Leu Ile Gly Asp Lys Gly

1

5

10

15

Val Ile Glu Ile Leu Ser Phe Leu Arg Phe Thr Thr Val Trp Asn Pro

20

25

30

Gly Ile Ser Phe Gly Ile Leu Asn Asn Phe Glu Tyr Ser Asn Val Val

35

40

45

Phe Cys Ser Ile Ser Ile Leu Ile Thr Cys Val Leu Cys Tyr Leu Phe

50

55

60

Ile Val Gln Pro His Tyr Arg Leu Pro Leu Val Ile Ile Ile Gly Gly

65

70

75

80

Ser Ile Gly Asn Ile Ile Asp Arg Ile Arg Tyr Gly Ala Val Tyr Asp

85

90

95

Phe Ile Asp Phe Tyr Ile Asn Asn Leu His Trp Pro Val Phe Asn Leu

100

105

110

Ala Asp Ser Phe Ile Phe Leu Gly Ile Val Ile Ile Met Ala Lys Ser

115

120

125

Asn Asn His Met Lys Gln Ile Asn Cys Asn Ser

130

135

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligonucleotide

<400> 12

aggcttggttc agggtgaaga agaatccaaac gacaaaagct t

41

<210> 13

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligonucleotide

<400> 13

aagcttttgt cgttggattc ttcttcaccc tgaacttgcc a

41